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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/910,695

DATE: 08/15/2001
 TIME: 13:37:04

Input Set : N:\Crf3\RULE60\09910695.txt
 Output Set: N:\CRF3\08152001\I910695.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: Hedrick, Joseph A.
 7 Vicari, Alain P.
 8 Zlotnik, Albert
 10 (ii) TITLE OF INVENTION: Mammalian Chemokines; Receptors;
 11 Reagents; Uses
 13 (iii) NUMBER OF SEQUENCES: 10
 15 (iv) CORRESPONDENCE ADDRESS:
 16 (A) ADDRESSEE: DNAX Research Institute
 17 (B) STREET: 901 California Avenue
 18 (C) CITY: Palo Alto
 19 (D) STATE: California
 20 (E) COUNTRY: USA
 21 (F) ZIP: 94304-1104
 23 (v) COMPUTER READABLE FORM:
 24 (A) MEDIUM TYPE: Floppy disk
 25 (B) COMPUTER: IBM PC compatible
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 29 (vi) CURRENT APPLICATION DATA:
 C--> 30 (A) APPLICATION NUMBER: US/09/910,695
 C--> 31 (B) FILING DATE: 20-Jul-2001
 37 (C) CLASSIFICATION:
 34 (vii) PRIOR APPLICATION DATA:
 35 (A) APPLICATION NUMBER: 09/122,585
 36 (B) FILING DATE: 24-JUL-1998
 39 (viii) ATTORNEY/AGENT INFORMATION:
 40 (A) NAME: Ching, Edwin P.
 41 (B) REGISTRATION NUMBER: 34,090
 42 (C) REFERENCE/DOCKET NUMBER: DX0757
 44 (ix) TELECOMMUNICATION INFORMATION:
 45 (A) TELEPHONE: (650)852-9196
 46 (B) TELEFAX: (650)496-1200
 49 (2) INFORMATION FOR SEQ ID NO: 1:
 51 (i) SEQUENCE CHARACTERISTICS:
 52 (A) LENGTH: 179 base pairs
 53 (B) TYPE: nucleic acid
 54 (C) STRANDEDNESS: single
 55 (D) TOPOLOGY: linear
 57 (ii) MOLECULE TYPE: cDNA
 60 (ix) FEATURE:
 61 (A) NAME/KEY: CDS
 62 (B) LOCATION: 18..179
 64 (x) PUBLICATION INFORMATION:
 65 (H) DOCUMENT NUMBER: US 60/053,693
 66 (I) FILING DATE: 25-JUL-1997

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68      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69      GTTAAACCAC ACTATTC ATG CAA AAG GGT GTA GGG TTA CTG AGG ACA GTT      50
70      Met Gln Lys Gly Val Gly Leu Leu Arg Thr Val
71      1 5 10
72      CCC TTG GTA CCT TCA GTC TCT GGT CAG ATT GAC CTT TTG GTA CTG TGT      98
73      Pro Leu Val Pro Ser Val Ser Gly Gln Ile Asp Leu Leu Val Leu Cys
74      15 20 25
75      ATG TGT ATA AAA ACG ACT ACT CCT CAT ATA TTT ATT TCT GAT TAT AAG      146
76      Met Cys Ile Lys Thr Thr Thr Pro His Ile Phe Ile Ser Asp Tyr Lys
77      30 35 40
78      ATA ATA TAT TCT GGA AAA CAC TGG AAA ATA CAT      179
79      Ile Ile Tyr Ser Gly Lys His Trp Lys Ile His
80      45
81      (2) INFORMATION FOR SEQ ID NO: 2:
82      (i) SEQUENCE CHARACTERISTICS:
83      (A) LENGTH: 54 amino acids
84      (B) TYPE: amino acid
85      (D) TOPOLOGY: linear
86      (ii) MOLECULE TYPE: protein
87      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
88      Met Gln Lys Gly Val Gly Leu Leu Arg Thr Val Pro Leu Val Pro Ser
89      1 5 10 15
90      Val Ser Gly Gln Ile Asp Leu Leu Val Leu Cys Met Cys Ile Lys Thr
91      20 25 30
92      Thr Thr Pro His Ile Phe Ile Ser Asp Tyr Lys Ile Ile Tyr Ser Gly
93      35 40 45
94      Lys His Trp Lys Ile His
95      50
96      (2) INFORMATION FOR SEQ ID NO: 3:
97      (i) SEQUENCE CHARACTERISTICS:
98      (A) LENGTH: 1314 base pairs
99      (B) TYPE: nucleic acid
100      (C) STRANDEDNESS: single
101      (D) TOPOLOGY: linear
102      (ii) MOLECULE TYPE: cDNA
103      (ix) FEATURE:
104      (A) NAME/KEY: CDS
105      (B) LOCATION: 179..1171
106      (x) PUBLICATION INFORMATION:
107      (H) DOCUMENT NUMBER: US 60/053,693
108      (I) FILING DATE: 25-JUL-1997
109      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
110      GTCTAAAACA AAATACAACA TTTCTTAAAT AACTGTTC CAGAAAGAGC TATTTTAAACA      60
111      GAAGCAACTC AAAGATATCC CTTCGACAGA AGTGGAAGTG CTGAAAAATG CTCATCTCTC      120
112      ACACAGACTT TTGATGGACA GGAGTTTCTA AGTATCATGC CTACCAACAA GCTGTAAA      178
113      ATG ATC ACC CTG AAC AAT CAA GAT CAA CCT GTC CCT TTT AAC AGC TCA      226
114      Met Ile Thr Leu Asn Asn Gln Asp Gln Pro Val Pro Phe Asn Ser Ser
115      1 5 10 15
116      CAT CCA GAT GAA TAC AAA ATT GCA GCC CTT GTC TTC TAT AGC TGT ATC      274

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142	His	Pro	Asp	Glu	Tyr	Lys	Ile	Ala	Ala	Leu	Val	Phe	Tyr	Ser	Cys	Ile	
143				20					25					30			
145	TTC	ATA	ATT	GGA	TTA	TTT	GTT	AAC	ATC	ACT	GCA	TTA	TGG	GTT	TTC	AGT	322
146	Phe	Ile	Ile	Gly	Leu	Phe	Val	Asn	Ile	Thr	Ala	Leu	Trp	Val	Phe	Ser	
147			35					40					45				
149	TGT	ACC	ACC	AAG	AAG	AGA	ACC	ACG	GTA	ACC	ATC	TAT	ATG	ATG	AAT	GTG	370
150	Cys	Thr	Thr	Lys	Lys	Arg	Thr	Thr	Val	Thr	Ile	Tyr	Met	Met	Asn	Val	
151		50					55					60					
153	GCA	TTA	GTG	GAC	TTG	ATA	TTT	ATA	ATG	ACT	TTA	CCC	TTT	CGA	ATG	TTT	418
154	Ala	Leu	Val	Asp	Leu	Ile	Phe	Ile	Met	Thr	Leu	Pro	Phe	Arg	Met	Phe	
155	65					70					75					80	
157	TAT	TAT	GCA	AAA	GAT	GCA	TGG	CCA	TTT	GGA	GAG	TAC	TTC	TGC	CAG	ATT	466
158	Tyr	Tyr	Ala	Lys	Asp	Ala	Trp	Pro	Phe	Gly	Glu	Tyr	Phe	Cys	Gln	Ile	
159				85						90				95			
161	ATT	GGA	GCT	CTC	ACA	GTG	TTT	TAC	CCA	AGC	ATT	GCT	TTA	TGG	CTT	CTT	514
162	Ile	Gly	Ala	Leu	Thr	Val	Phe	Tyr	Pro	Ser	Ile	Ala	Leu	Trp	Leu	Leu	
163			100						105				110				
165	GCC	TTT	ATT	AGT	GCT	GAC	AGA	TAC	ATG	GCC	ATT	GTA	CAG	CCG	AAG	TAC	562
166	Ala	Phe	Ile	Ser	Ala	Asp	Arg	Tyr	Met	Ala	Ile	Val	Gln	Pro	Lys	Tyr	
167			115						120				125				
169	GCC	AAA	GAA	CTT	AAA	AAC	ACG	TGC	AAA	GCC	GTG	CTG	GCG	TGT	GTG	GGA	610
170	Ala	Lys	Glu	Leu	Lys	Asn	Thr	Cys	Lys	Ala	Val	Leu	Ala	Cys	Val	Gly	
171		130					135					140					
173	GTC	TGG	ATA	ATG	ACC	CTG	ACC	ACG	ACC	ACC	CCT	CTG	CTA	CTG	CTC	TAT	658
174	Val	Trp	Ile	Met	Thr	Leu	Thr	Thr	Thr	Thr	Pro	Leu	Leu	Leu	Leu	Tyr	
175	145					150					155					160	
177	AAA	GAC	CCA	GAT	AAA	GAC	TCC	ACT	CCC	GCC	ACC	TGC	CTC	AAG	ATT	TCT	706
178	Lys	Asp	Pro	Asp	Lys	Asp	Ser	Thr	Pro	Ala	Thr	Cys	Leu	Lys	Ile	Ser	
179				165						170				175			
181	GAC	ATC	ATC	TAT	CTA	AAA	GCT	GTG	AAC	GTG	CTG	AAC	CTC	ACT	CGA	CTG	754
182	Asp	Ile	Ile	Tyr	Leu	Lys	Ala	Val	Asn	Val	Leu	Asn	Leu	Thr	Arg	Leu	
183			180							185				190			
185	ACA	TTT	TTT	TTC	TTG	ATT	CCT	TTG	TTC	ATC	ATG	ATT	GGG	TGC	TAC	TTG	802
186	Thr	Phe	Phe	Phe	Leu	Ile	Pro	Leu	Phe	Ile	Met	Ile	Gly	Cys	Tyr	Leu	
187			195					200					205				
189	GTC	ATT	ATT	CAT	AAT	CTC	CTT	CAC	GGC	AGG	ACG	TCT	AAG	CTG	AAA	CCC	850
190	Val	Ile	Ile	His	Asn	Leu	Leu	His	Gly	Arg	Thr	Ser	Lys	Leu	Lys	Pro	
191		210					215					220					
193	AAA	GTC	AAG	GAG	AAG	TCC	ATA	AGG	ATC	ATC	ATC	ACG	CTG	CTG	GTG	CAG	898
194	Lys	Val	Lys	Glu	Lys	Ser	Ile	Arg	Ile	Ile	Ile	Thr	Leu	Leu	Val	Gln	
195	225					230					235					240	
197	GTG	CTC	GTC	TGC	TTT	ATG	CCC	TTC	CAC	ATC	TGT	TTC	GCT	TTC	CTG	ATG	946
198	Val	Leu	Val	Cys	Phe	Met	Pro	Phe	His	Ile	Cys	Phe	Ala	Phe	Leu	Met	
199				245						250				255			
201	CTG	GGA	ACG	GGG	GAG	AAC	AGT	TAC	AAT	CCC	TGG	GGA	GCC	TTT	ACC	ACC	994
202	Leu	Gly	Thr	Gly	Glu	Asn	Ser	Tyr	Asn	Pro	Trp	Gly	Ala	Phe	Thr	Thr	
203			260							265				270			
205	TTC	CTC	ATG	AAC	CTC	AGC	ACG	TGT	CTG	GAT	GTG	ATT	CTC	TAC	TAC	ATC	1042
206	Phe	Leu	Met	Asn	Leu	Ser	Thr	Cys	Leu	Asp	Val	Ile	Leu	Tyr	Tyr	Ile	

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207          275          280          285
209 GTT TCA AAA CAA TTT CAG GCT CGA GTC ATT AGT GTC ATG CTA TAC CGT      1090
210 Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr Arg
211          290          295          300
213 AAT TAC CTT CGA AGC ATG CGC AGA AAA AGT TTC CGA TCT GGT AGT CTA      1138
214 Asn Tyr Leu Arg Ser Met Arg Arg Lys Ser Phe Arg Ser Gly Ser Leu
215 305          310          315          320
217 CGG TCA CTA AGC AAT ATA AAC AGT GAA ATG TTA TGAATAATAA GGTTCTTTCA      1191
218 Arg Ser Leu Ser Asn Ile Asn Ser Glu Met Leu
219          325          330
221 TTTCAATCCC ATCAAAATTC ACTTCACTAA CTACTCTGGC GTCAATGGAT ATTCTGTATA      1251
223 ATACTATCAA GTCCCTTTTC TCTTGAAAAA ATAAATTCAT TATCTTCATT TTAAAAACTT      1311
225 AAA      1314
228 (2) INFORMATION FOR SEQ ID NO: 4:
230 (i) SEQUENCE CHARACTERISTICS:
231 (A) LENGTH: 331 amino acids
232 (B) TYPE: amino acid
233 (D) TOPOLOGY: linear
235 (ii) MOLECULE TYPE: protein
237 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
239 Met Ile Thr Leu Asn Asn Gln Asp Gln Pro Val Pro Phe Asn Ser Ser
240 1 5 10 15
242 His Pro Asp Glu Tyr Lys Ile Ala Ala Leu Val Phe Tyr Ser Cys Ile
243 20 25 30
245 Phe Ile Ile Gly Leu Phe Val Asn Ile Thr Ala Leu Trp Val Phe Ser
246 35 40 45
248 Cys Thr Thr Lys Lys Arg Thr Thr Val Thr Ile Tyr Met Met Asn Val
249 50 55 60
251 Ala Leu Val Asp Leu Ile Phe Ile Met Thr Leu Pro Phe Arg Met Phe
252 65 70 75 80
254 Tyr Tyr Ala Lys Asp Ala Trp Pro Phe Gly Glu Tyr Phe Cys Gln Ile
255 85 90 95
257 Ile Gly Ala Leu Thr Val Phe Tyr Pro Ser Ile Ala Leu Trp Leu Leu
258 100 105 110
260 Ala Phe Ile Ser Ala Asp Arg Tyr Met Ala Ile Val Gln Pro Lys Tyr
261 115 120 125
263 Ala Lys Glu Leu Lys Asn Thr Cys Lys Ala Val Leu Ala Cys Val Gly
264 130 135 140
266 Val Trp Ile Met Thr Leu Thr Thr Thr Thr Pro Leu Leu Leu Tyr
267 145 150 155 160
269 Lys Asp Pro Asp Lys Asp Ser Thr Pro Ala Thr Cys Leu Lys Ile Ser
270 165 170 175
272 Asp Ile Ile Tyr Leu Lys Ala Val Asn Val Leu Asn Leu Thr Arg Leu
273 180 185 190
275 Thr Phe Phe Phe Leu Ile Pro Leu Phe Ile Met Ile Gly Cys Tyr Leu
276 195 200 205
278 Val Ile Ile His Asn Leu Leu His Gly Arg Thr Ser Lys Leu Lys Pro
279 210 215 220
281 Lys Val Lys Glu Lys Ser Ile Arg Ile Ile Ile Thr Leu Leu Val Gln

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282 225          230          235          240
284 Val Leu Val Cys Phe Met Pro Phe His Ile Cys Phe Ala Phe Leu Met
285          245          250          255
287 Leu Gly Thr Gly Glu Asn Ser Tyr Asn Pro Trp Gly Ala Phe Thr Thr
288          260          265          270
290 Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Ile Leu Tyr Tyr Ile
291          275          280          285
293 Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr Arg
294          290          295          300
296 Asn Tyr Leu Arg Ser Met Arg Arg Lys Ser Phe Arg Ser Gly Ser Leu
297 305          310          315          320
299 Arg Ser Leu Ser Asn Ile Asn Ser Glu Met Leu
300          325          330
302 (2) INFORMATION FOR SEQ ID NO: 5:
304     (i) SEQUENCE CHARACTERISTICS:
305         (A) LENGTH: 400 base pairs
306         (B) TYPE: nucleic acid
307         (C) STRANDEDNESS: single
308         (D) TOPOLOGY: linear
310     (ii) MOLECULE TYPE: cDNA
313     (ix) FEATURE:
314         (A) NAME/KEY: CDS
315         (B) LOCATION: 2..226
317     (x) PUBLICATION INFORMATION:
318         (H) DOCUMENT NUMBER: US 60/053,693
319         (I) FILING DATE: 25-JUL-1997
321     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
323 G CTA CAA GGA CAG GAG AAC AGC TAT AGC CCC TGG GGA GCC TTC ACC      46
324   Leu Gln Gly Gln Glu Asn Ser Tyr Ser Pro Trp Gly Ala Phe Thr
325       1          5          10          15
327 ACC TTC CTC ATG AAC CTC AGC ACC TGT CTC GAT GTA GTC CTC TAC TAC      94
328 Thr Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Val Leu Tyr Tyr
329       20          25          30
331 ATC GTT TCC AAA CAG TTC CAG GCT CGA GTC ATC AGC GTC ATG CTG TAC     142
332 Ile Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr
333       35          40          45
335 CGC AAT TAC CTT CGC AGT GTT CGC AGA AAA AGT GTC CGA TCG GGC AGT     190
336 Arg Asn Tyr Leu Arg Ser Val Arg Arg Lys Ser Val Arg Ser Gly Ser
337       50          55          60
339 TTA CGG TCA CTT AGC AAC ATG AAC AGT GAG ATG CTT TGAGTCAGAG      236
340 Leu Arg Ser Leu Ser Asn Met Asn Ser Glu Met Leu
341       65          70          75
343 CAAGCTGCCA GTCTTCAGTC TCTTTAAAAT TCTTTTCCTA TCTACTTTCG GGTGAACCAG     296
345 CATTCTACAC TATCCAGTCC CTTCTCTAAC AAAGAGAAAT AATAATGATG AACTTTAAAA     356
347 ACTTCTGCGG TATTCTGTGT ATTCTAGCCA CATGATTAAA AACT      400
350 (2) INFORMATION FOR SEQ ID NO: 6:
352     (i) SEQUENCE CHARACTERISTICS:
353         (A) LENGTH: 75 amino acids
354         (B) TYPE: amino acid

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09910695.txt

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]